## Isolation of X and Y Chromosome-Specific DNA Markers From a Liverwort, Marchantia polymorpha, by Representational Difference Analysis

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#### ABSTRACT

The liverwort *Marchantia polymorpha* has X and Y chromosomes in the respective female and male haploids. Here we report the successful exploitation of representational difference analyses to isolate DNA markers for the sex chromosomes. Two female-specific and six male-specific DNA fragments were genetically confirmed to originate from the X and Y chromosomes, respectively.

In a few dioecious plants, morphologically distinct sex chromosomes (Ainsworth et al. 1998; Juarez and Banks 1998), which are expected to play a crucial role in sex determination and differentiation, have been observed. Thus far, several repeated sequences and a few genes have been isolated from sex chromosomes of two plant species: Silene latifolia (Donnison et al. 1996; Bužek et al. 1997; Scutt et al. 1997; Guttman and Charlesworth 1998; Delichére et al. 1999; Matsunaga et al. 1999) and Rumex acetosa (Shibata et al. 1999). However, the molecular function of sex chromosomes in sex determination and differentiation in plants still remains largely unknown.

The liverwort *Marchantia polymorpha* is dioecious and haploid during most of its life cycle. *M. polymorpha* has an X chromosome in female and a Y chromosome in male individuals, in addition to the common eight autosomes (BISCHLER 1986). This X/Y exclusiveness can be exploited to isolate sex chromosome-specific DNA fragments for both of the sex chromosomes. In contrast, in most dioecious plants, DNA fragments unique to an X chromosome cannot be readily identified because the X chromosome is present in both males and females.

We previously isolated a P1-derived artificial chromosome (PAC) clone specific to the Y chromosome, pMM-4G7, from the male genomic library of *M. polymorpha* (OKADA *et al.* 2000). Furthermore, we found that the sequences cloned in pMM4G7 have accumulated in a distinct region of the Y chromosome (OKADA *et al.* 2001). The X chromosome, on the other hand, carries 17S rDNA sequences (NAKAYAMA *et al.* 2001). The sequence composition of the other regions of the Y and X chromosomes, respectively, has remained unclear.

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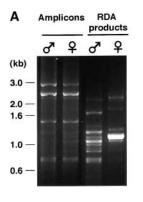
To obtain DNA markers unique to these sex chromosomes in *M. polymorpha*, we performed representational difference analysis (RDA) using male and female total DNAs digested with *Bam*HI, *Hin*dIII, or *BgI*II.

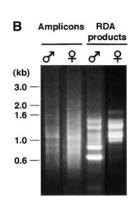
#### MATERIALS AND METHODS

**Plant materials:** Female and male thalli of M. polymorpha (E lines; Okada  $et\ al.\ 2000$ ) were used for RDA and as parents for linkage analysis.  $F_1$  progenies were generated by crossing male and female individuals as follows: sperm cells were collected by adding sterilized water onto a male sex organ and then recovering the water, which was poured onto a female sex organ 5 mm in height. The resulting spores were cultivated in the conditions described by Okada  $et\ al.\ (2000)$ .

Representational difference analysis: The RDA procedure was essentially as described by LISITSYN et al. (1993). Briefly, amplicons were generated from 1 µg of male and female total DNA, respectively. Adaptors were removed from tester and driver by ultrafiltration (SUPREC-02, Takara Biomedicals, Kusatsu, Japan) after digestion with the respective restriction enzymes. Tester was ligated to the J-adaptor for the first and third RDA rounds, and the N-adaptor for the second and fourth rounds. A mixture of tester and driver in 8 µl of 30 mм N-(2-hydroxyethyl)piperazine-N'-(3-propanesulfonic acid) and 3 mm EDTA (pH 8.0) (STRAUS and AUSUBEL 1990) overlaid with 35 µl of mineral oil (Sigma-Aldrich, Steinheim, Germany) was denatured at 98° for 5 min; 2  $\mu l$  of 5 M NaCl was then added, and the DNA was allowed to hybridize at 67° for 36 hr. Forty micrograms of the driver DNA was used for each round, while the tester DNA was added in the following amounts: when RDA was performed with BamHI or Bg/III, 400 ng tester was added for the first round, 50 ng for the second, and 100 pg for the third; with HindIII, 400 ng tester was added for the first round, 100 ng for the second, 400 pg for the third, and 5 pg for the fourth. To the subtractions with amplicons from the female DNA as driver and with amplicons from the male DNA as tester, 1 µg DNA from pMM4G7 was added to the driver preparation to eliminate those Y chromosomespecific repetitive sequences (Okada et al. 2000, 2001) from the male tester DNA.

PCR assay: Twenty nanograms of *M. polymorpha* total DNA was amplified in a 20-µl reaction containing 0.5 units of AmpliTaqGold (Applied Biosystems, Foster City, CA), 2 mm of MgCl<sub>2</sub>,





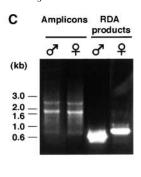


FIGURE 1.—RDA products from *M. polymorpha* male and female genomic DNA digested with *Bam*HI (A), *Hind*III (B), and *BgI*II (C), respectively. The third-round RDA products (A and C) and the fourth-round RDA products (B) were electrophoresed.

 $0.5~\mu m$  of each primer, and 0.2~mm of each dNTP. PCR cycles were programmed as follows: 10~min at  $96^\circ$  followed by 35 cycles ( $96^\circ$  for 1~min,  $50–54^\circ$  for 1~min, according to the melting temperature of respective primers sets, and  $72^\circ$  for 1~min) with a GeneAmp PCR System 9700 (Applied Biosystems). The primers, which can detect a sequence present in both male and female (CDPK-Ex1; Nishiyama  $\it et~al.~1999$ ), were used as a positive confirmation of male and female PCR amplifications (Okada  $\it et~al.~2000$ ), and the Y-specific primers for 4G7-T7 were used to score the male sex of progeny individuals (Okada  $\it et~al.~2000$ ).

Screening and aligning Y chromosome-derived PAC clones: PAC clones were screened from the *M. polymorpha* male genomic PAC library (OKADA *et al.* 2000) by PCR assay with pooled PAC DNA (GREEN and OLSON 1990; CHINAULT 1994) using primers for rbm27 (see below) under the same conditions as described above. Plasmid DNA of the PAC clones and the rbm27 were digested with *Bam*HI and electrophoresed in 0.7% agarose gel with 1× TAE buffer, and then the gel was stained by SYBR Gold (Molecular Probes, Eugene, OR) to confirm that the RDA-derived fragment was carried by the PAC clone and to align the PAC clones. The overlap of PAC clones was also confirmed by PCR amplification with each PAC DNA as template, using respective sets of primers for the SP6 and T7 ends of pMM23-104E4 (termed esM104E4, 5'-GGACTCTTCG CAGTCATGTATTC and 5'-CCTGGTATTACGAGAGAGCT

GAAC; etM104E4, 5'-TCCTTGCCGTGAGAGTTGATGTTC and 5'-AGAGAAGGATTGGGAGCCATTGATT). The PCR condition was described above.

The sequence data presented in this article have been submitted to the DDBJ/EMBL/GenBank Data Libraries under accession nos. AB069714 for rbm27, AB069720 for rhm12, AB069780 for rhm13, AB069718 for rgm6, AB069717 for rgm29, AB069716 for rgm108, AB069715 for rbf62, and AB069719 for rhf73, and the SP6- and T7-end sequences of the DNA fragment cloned into pMM23-104E4 [104E4SP6 (AB069721) and 104E4T7 (AB069722)].

#### RESULTS AND DISCUSSION

Isolation of DNA fragments specific to the male or female by RDA: Although initial male and female amplicons were visually indistinguishable from each other, DNA fragments unique to male or female plants were observed in the third-round products of *BamHI*, the fourth-round products of *HindIII*, and the third-round products of *BglII* (Figure 1, A–C). These differences between male and female RDA products reflect the potential enrichment of DNA fragments characteristic of

TABLE 1
List of sex chromosome-specific RDA clones

Clone	Insert DNA size (bp)	${ m Linkage}^a$	Primer	Amplification size (bp)
rbm27 (BamHI)	1202	Y	Forward CCAAGTGCGGGCAGAATCAAGT	663
			Reverse TTCATCGCCCGCTATCACCTTC	
rhm12 ( <i>Hin</i> dIII)	1000	Y	Forward GAGAGTATTTGCGATGCGTCAC	476
			Reverse CAAGGGCTCGAATCCATTTCT	
rhm13 ( <i>Hin</i> dIII)	1131	Y	Forward ACGTTGACGCATAAGGACATAA	310
			Reverse ATACCGGAAGGCATTTCATC	
rgm6 (BglII)	899	Y	Forward TATCTCCGGGACATCTTTCTCTCT	211
			Reverse TCTCTATGAGGGGATTTTATTATT	
rgm29 (BglII)	221	Y	Forward CGCTGTCCAATCTTTCAAATAA	197
			Reverse ACAGCGGAGAACTGACTGACCC	
rgm108 (BglII)	658	Y	Forward GGAGACCTCTATCACCGCTGAAACT	361
			Reverse CACCTGCGGAGACTTATCTTACCTG	
rbf62 (BamHI)	2444	X	Forward CAATTGGGAAGATTTGACACTTAGC	454
			Reverse TTCCCAATTGAGTACGAGTAGTCCT	
rhf73 ( <i>Hin</i> dIII)	1075	X	Forward TGACGACGAAGATGTGGATGAC	406
			Reverse GAAACTTGGCCGTGTGACTGA	

<sup>&</sup>lt;sup>a</sup>Y, Y linked; X, X linked.

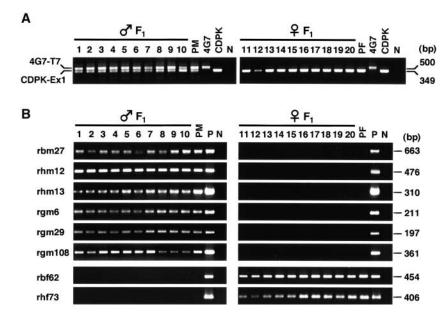


FIGURE 2.—Genetic linkage analysis of RDAderived clones. (A) Sex of the  $F_1$  progenies. Ten male individuals (left) and 10 females (right) were identified in the F1. Lanes PM and PF, genomic DNA from parental male and female individuals; lanes 4G7 and CDPK, positive controls for respective primers; lane N, without template for a negative control. (B) Segregation of RDA-derived clones in the male and female F<sub>1</sub> progeny. Lanes 1-10, male F<sub>1</sub> progeny individuals; lanes 11-20, female F<sub>1</sub> progeny individuals. Lanes PM and PF, genomic DNA from parental male and female individuals. Lane P, the respective RDA-derived clones as template for a positive control. Lane N, without template for a negative control.

the male or the female genomes and therefore were investigated further.

The RDA products from the male and female genomic DNA were cloned into a cloning vector pBluescript II SK+ with the respective restriction enzymes and sequenced. For identification of male-specific RDA clones, 41 primer sets for the male RDA-derived clones (12 primer sets for *Bam*HI-RDA clones, 24 for *Hin*dIII-RDA clones, and 5 for *BgI*II-RDA clones) were designed; for identification of female-specific RDA clones, 67 primer sets for the female RDA-derived clones (9 for *Bam*HI-

RDA clones, 53 for *Hin*dIII-RDA clones, and 5 for *BgI*II-RDA clones) were designed. PCR test amplifications were performed on male and female genomic DNAs using each of these primer sets to determine whether the RDA-derived DNA fragments are indeed specific to either the parental male or female. Seven primer sets for male RDA-derived clones (2 for *Bam*HI-RDA clones, 2 for *Hin*dIII-RDA clones, and 3 for *BgI*II-RDA clones) yielded PCR products in the parental male only and not in the parental female DNA (data not shown); 6 primer sets for female RDA-derived clones (2 for *Bam*HI-RDA

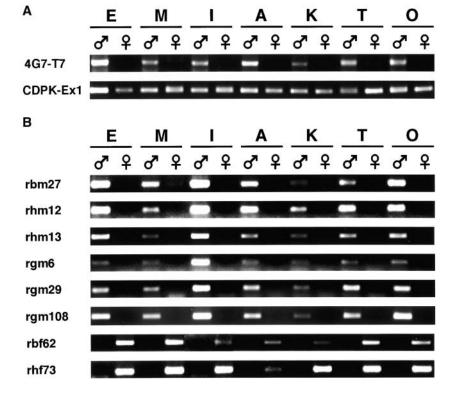


FIGURE 3.—Sex specificity of RDA-derived clones in the wild *M. polymorpha*. (A) Male specificity of the primers for 4G7-T7. (B) Sex specificity of RDA-derived clones. Lines E, M, I, A, K, T, and O were collected from different places in Japan. Lines E, M, and I were described by OKADA *et al.* (2000). The sex of these lines was checked by the presence of male or female sex organs.

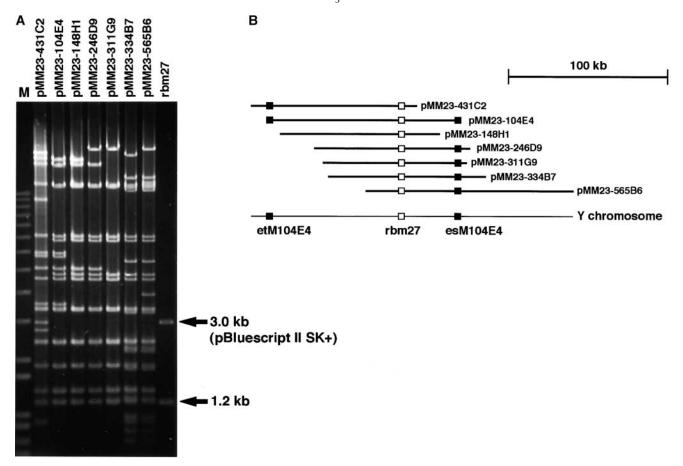


FIGURE 4.—PAC clones isolated by the primers for rbm27 as a marker. (A) Agarose gel electrophoresis of PAC clones. Arrows indicate the RDA-derived DNA fragment of rbm27 (1.2 kb) and a cloning vector pBluescriptII SK+ (3.0 kb), respectively. Lane M is the 1-kb plus DNA ladder (GIBCO BRL, Rockville, MD). (B) A PAC contig map of the region containing rbm27 on the Y chromosome. PAC clones are indicated by labeled horizontal lines. Open squares indicate the amplification found with each PAC DNA as template by PCR using a set of primers for rbm27. Solid squares indicate the amplification found with each PAC DNA as template by PCR using respective sets of primers for the SP6- and T7-ends of pMM23-104E4 (termed esM104E4 and etM104E4, respectively). The exact position of rbm27 in each PAC clone and the location of the contig on the Y chromosome are undefined.

clones, 3 for *Hin*dIII-RDA clones, and 1 for the *BgI*II-RDA clone) amplified a product from the parental female, but not the parental male, DNA (data not shown).

Identification of RDA-derived DNA fragments specific to the sex chromosomes by genetic linkage analysis: Since the male and female plants used for RDA in this study were collected from wild populations, it was necessary to test whether the seven male-derived primer sets and six female-derived primer sets we confirmed are indeed specific to the male and female sex chromosomes, respectively. To do this, we performed cosegregation analysis using male and female F<sub>1</sub> progeny individuals. These were generated by crossing the male and female parents used for RDA isolation, and the sex of progeny plant was determined using PCR with the malespecific primer set 4G7-T7 (OKADA et al. 2000). We also tested six more pairs of wild M. polymorpha collected from different localities in Japan and found that only male individuals were positive (Figure 3A), indicating that 4G7-T7 can be used for determining the sex of M.

polymorpha individuals. A total of 10 male and 10 female individuals from the F<sub>1</sub> family were used for linkage analysis. The primer sets for six male RDA-derived clones, termed rbm27, rhm12, rhm13, rgm6, rgm29, and rgm108 (Table 1), showed amplification only in the 10 male progeny, not in the females (Figure 2B). On the other hand, the primer sets for two female RDA-derived clones, termed rbf62 and rhf73 (Table 1), showed amplification only in the 10 females (Figure 2B). These results are statistically highly significant evidence for linkage. Using the genomic DNAs from wild M. polymorpha plants as templates, the above primer sets were further confirmed to be sex specific (Figure 3B).

Sequence analysis of the RDA-derived DNA fragments specific to the sex chromosomes: The nucleotide sequences of the six Y chromosome-specific DNA fragments (rbm27, rhm12, rhm13, rgm6, rgm29, and rgm108) showed no significant similarities to known sequences registered in the public databases as searched by BLAST (ALTSCHUL *et al.* 1997). Furthermore, none of these

Y chromosome-specific sequences display an extended reading frame, suggesting that they are not derived from protein-coding regions.

The nucleotide sequence of the X chromosome-specific DNA fragment rbf62 contains a 5S rRNA gene, indicating that this gene is present in the X chromosome as well as in the autosomes. Sone et al. (1999) reported the presence of the 5S rRNA gene in the 45S rDNA unit of M. polymorpha, and NAKAYAMA et al. (2001) showed that an rDNA cluster is found on the X chromosome, but not on the Y chromosome. The flanking regions of the 5S rRNA gene sequence in rbf62 are different from the rDNA unit previously reported (Sone et al. 1999), and it is not clear whether the rDNA unit was derived from autosomes or from the X chromosome. The linkage of rbf62 to the X chromosome implies that the flanking regions of the 5S rRNA gene sequence on the X chromosome have evolved differences from the autosomal units.

The nucleotide sequence of another X-linked sequence, rhf73, is found in two *M. polymorpha* expressed sequence tags (ESTs), F011154 and F01Q066 (GenBank accession nos. C96067 and C96366, respectively), which had been isolated from immature female sex organs (NAGAI *et al.* 1999). Neither the rhf73 nor the two ESTs show similarity to sequences registered in the public databases.

The utility of RDA-derived DNA fragments as markers: To apply RDA-derived DNA fragments as markers to isolation of larger genomic DNA fragments, PAC clones from a male genomic library (Okada et al. 2000) were screened by PCR using a set of primers for one of the Y chromosome-specific DNA fragments, rbm27. Seven PAC clones were isolated from the male genomic PAC library, which contains 22,000 clones. The cloning frequency of rbm27 (1 out of  $\sim$ 3000 clones) suggests that this sequence is present as a single genomic locus, since this library covers the male genome sevenfold (Okada et al. 2000). A contig map of these PAC clones was constructed from their restriction profiles and the PCR amplification, using sets of primers for both end sequences of one of the PAC clones, pMM23-104E4. The map indicates that these PAC clones cover a single common overlapping region of the genome, thus further substantiating that rbm27 is derived from a unique Y chromosome locus (Figure 4, A and B).

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